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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                            Minimum
Maximum
                                                                                                                                                                                                                               Database
                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 10
Listing first 45
                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on:
                                                                                                                                                                                                                                                                                                            DB
Bd
                                                                                                                                                                                                                                                                                                           seq length: 0 seq length: 2000000000
                                                                                                    SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1
9: sp_phage:*
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1 APPPNLPDPKFESKA
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Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                           APPPNLPDPKFESKAALLAA......GGFWSAWSEPVSLLTPSDLD
sp_vodent:*
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45 summaries
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	000	7	6	· U	4	· w	N		Result No.	
137	139	140	140.5	151	157.5	159	159.5	160.5	185	778.5	778.5	846	851	965.5	1005.5	Score	
11.5	11.6	11.7	11.8	12.6	13.2	13.3	13.4	13.4	15.5	65.2	65.2	70.9	71.3	80.9	84.2	Query Match Length	d
622	625	227	626	581	425	296	422	422	566	418	387	229	229	316	509	Length 1	
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Q9N0J7	Q9XS92	Q9GLW3	Q90WG7	046561	Q9JM58	018880	Q9UHH5	075462	Q925F5	Q95N14	Q95N13	Q28206	Q27950	035545	Q9WYZ9	ID	
Q9n0j7 callithrix	Q9xs92 trichosurus	Q9glw3 ursus marit	Q90wg7 cynops pyrr	046561 ovis aries	Q9jm58 mus musculu	018880 bos taurus	Q9uhh5 homo sapien	075462 homo sapien	Q925f5 mus musculu	Q95n14 ovis aries	Q95n13 ovis aries	Q28206 bos taurus	Q27950 bos indicus	035545 rattus norv	Q9myz9 sus scrofa	Description	

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ALIGNMENTS

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Q9MYZ9 PRELIMINARY;
Q9MYZ9;
01-OCT-2000 (TrEMBLrel. 15, C
01-OCT-2000 (TrEMBLrel. 15, I
01-DEC-2001 (TrEMBLrel. 19, I
ERYTHROPOIETIN RECEPTOR.
 PROSITE;
PROSITE;
Receptor.
SEQUENCE
                                                                                                                                        TISSUE=LIVER; Pearson P.L., Smith T.P.L., Sonstegard T.S., Klemcke H.G., Christenson R.K., Vallet J.L.; Christenson R.K., Vallet J.L.;
                                                                                                                                                                                                            Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                           "Porcine Erythropoietin Receptor: Molecular Cloning and Expression in Embryonic and Fetal Liver."; Domest. Anim. Endocrinol. 0:00-0(2000). EMBL; AF274305; AAF77065.1; -.
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                   NCBI_TaxID=9823;
  509 AA; 55183 MW; 35B565D07C6BCD8A CRC64;
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Query Match
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InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hematopo_receptor_L_F1.
InterPro; IPR003528; Hematopo_receptor_L_F1.
SMART; SM00060; FN3; 1.
PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-98296111; PubMed-9630610;
Murakami C., Takenoshita
                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; Receptor. SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressed as a membrane-bound form.";
Biochim. Biophys. Acta 1403:169-178(1998).
EMBL; D83509; BAA22373.1; -.
HSSP; P19235; 1EBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
10TRON 5-INSERTED FORM OF ERYTHROPOIETIN RECEPTOR P
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intron 5-inserted form of rat erythropoietin
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                                                              CVLSNLRGGTRYTFAVRARMAEPSFSGFWSAWSEPASLLTAS
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82.4%;
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Pred. No. 5.
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Submitted (JUN-1996) to the E
EMBL; U61398; AAB03870.1; -.
HSSP; P19235; 1EBA.
InterPro; IPR002996; CR1A.
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SMART; SM00060; FN3; 1.
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TISSUE-BONE MARROW;
Suliman H.B., Feldman B.F.,
Submitted (JUN-1996) to the
EMBL; U61399; AAB03871.1; -.
HSSP; P19235; 1EBA.
                                                                                                                         Bos taurus (Bovine),
Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-DEC-2001 (TremBLrel.
ERYTHROPOIETIN RECEPTOR
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                                                                       SEQUENCE FROM N.A.
                                                                                                NCBI_TaxID=9913;
                                                                                                               Bovidae; Bovinae;
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                                                                                                                             Chordata; Craniata; Vertebrat
Cetartiodactyla; Ruminantia;
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                                                                                                                                                                                                  Created)
Last sequence update)
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                             Majiwa P.A.O., Logan-Henfrey EMBL/GenBank/DDBJ databases.
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EMBL/GenBank/DDBJ
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Best Local :
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CV1s aries (Sheep). Chordata; Craniata; Vert Enkaryota; Metazoa; Chordata; Craniata; Vert Control of the Control of t
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                           GNGAGSVQRVEILEGRTECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPS
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                                                                                    SSGASRYRRTIHVNEVVLLDPPARLVARRADEGGHVVLRWLPPPGAPMASLIRYEVNISA
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Pred.
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red. No. 2.8e
Mismatches
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2.8e-65;
les 26;
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les 24;
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Q925F5;
01-DEC-2001 (TrEMBLrel. 19, C
01-DEC-2001 (TrEMBLrel. 19, L
01-DEC-2001 (TrEMBLrel. 19, L
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SEQUENCE
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"Quantitation of the mRNA le
the ovine fetus.";
Submitted (APR-2001) to the
EMBL; AY029231; AAK38170.1;
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SEQUENCE FROM N.A.
Sabath D.F., Lofton-Day C., Lin N., Lok S., Ka
Broudy V.C.;
Independent of the Endly General Submitted (MAR-2001) to the EMBL/GenBank/DDBJ
EMBL; AF360122; AAK52492.1; -.
                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                                                                                                                                                                                       C-MPL-II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERYTHROPOIETIN RECEPTOR (FRAGMOVIS aries (Sheep).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovidae; Caprinae;
NCBI_TaxID=9940;
                                                                                                                                                 NCBI_TaxID=10090;
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Last sequence up
Last annotation
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075462;
01-NOV-1998
                                                                                                                                                                                                                  CHAIN
SEQUENCE
                                                                                                                                                                                                                                                     Signal;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                       Magrangeas F., Jacques Y., Minvielle S.; "Cloning and expression of a novel soluble prohematopoietic cytokine receptor domains."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ EMBL; AF059293; AAC28335.1; -. EMBL; AF073515; AAD39681.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Elson G.C.A., Graber P., Losberger P., Herren S., Gretener D., Menoud L.N., Wells T.N.C., Kosco-Vilbois M.H., Gauchat J.F.; "CLF-1, a Novel Soluble Protein Shares Homology With Members o Cytokine Type-I Receptor Family."; J. Immunol. 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLF-1.
Homo sapiens (Human).
Homo sapiens (Human).
'~rvota; Metazoa; Chordata;
'~rvota; Primates;
                                                                                                                                                                                                                                                                                  InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_II
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 2.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CYTOKINE-LIKE FACTOR-1 PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQDVFLLALGTEPLNCFSQTFEDLTCFWDEEEAA--PSGTYQLLYAYRGEKPRACPLYSQ
                    HQAPTARGAVRFWCSLPTADTSSFVPLELRVTAAS--GAPRYH-RVIHINEVVLLDAPVG
                                                       PVNISCWSKNMKDLTCRWT------PGAHGETFLHTNYSLKYKLR---WYGQDNTCEE
                                                                                        PEELLCFTERLEDLVCFWEEAASAGVGPG-----NYSFSYQLEDEPW----KLCRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPVLDQPPCVHPTASQPHGPV--RTSPAGEAPF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVPTFGTRYVCQFPAQDEVRLFFPLHLWVKNVSLNQTLIQRVLFVDSVETCCPTLWMPNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61;
                                                                                                                                                                                                                                                                     Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -CLVSGLQAGKSYWLQLRSQPDGVSLRGSWGPWSFPVTVDLPGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                            Similarity
                                                                                                                                                                                                                  38
422 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                  422 (
46301 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63339
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27.0%;
                                                                                                                                                                                                                                                                                                                 FN_III.
                                                                                                                                            13.4%; 26.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23;
                                                                                                                           29;
 -
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-
                                                                                                                         Score 160.5;
Pred. No. 5.8e
29; Mismatches
                                                                                                                                                                                                                POTENTIAL.
CYTOKINE-LIKE FACTOR-1
AD9DEFCB01B84228 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A19D3DD5F7BDBA6B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          422
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                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---LTVKGGS----
                                                                                                                                                                                                                                                                                                                                                                                                                                             protein containing
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                                                                                                                             84;
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                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                            Length 422;
                                                                                                                           Indels
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                                                                                                                           55;
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                                                                                                                           13;
018880
ID 01
AC 01
AC 01
DT 01
DT 01
DT 01
DT 01
OS BC
OC BC
OC BC
OX NC
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                018880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
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01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
             Bos taurus (Bovine).
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                           O18880;
01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lok S., Presnell S.R., Jelmberg A.C., Gilbert T., Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J., Submitted (AUG-1999) to the EMBL/GenBank/DDBJ date EMBL; AF178684; AAD54385.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003961;
Pfam; PF00041; fn3; 2
SMART; SM00060; FN3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASS I CYTOKINE RECEPTOR.
Bovidae; Bovinae; Bos.
                                                                           PROLACTIN RECEPTOR SHORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                         CVLSNLRGRTRYTFAVRARMAEPSFG------GFWSAWSEPVSLLTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEELLCFTERLEDLVCFWEEAASAGVGPG-----NYSFSYQLEDEPW----KLCRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRLAGLKPGTVYFVQVRCN----PFGIYGSKKAGIWSEWSHPTAASTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CVLSNLRGRTRYTFAVRARMAEPSFG-----GFWSAWSEPVSLLTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L-VARLADESGHVVLRWLPPPET-----PMTSHIRYEVDVSAGNGAGSVQRVEILEGRTE 180
: |:|: : | : : : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YHTVGPHS-----CHIP-KDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPD
                                                                                                                                                                                                                                                                     CRLAGLKPGTVYFVQVRCN----PFGIYGSKKAGIWSEWSHPTAASTP
                                                                                                                                                                                                                                                                                                                                               VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSV-----DWKVVDDVSNQTS
                                                                                                                                                                                                                                                                                                                                                                 L-VARLADESGHVVLRWLPPPET-----PMTSHIRYEVDVSAGNGAGSVQRVEILEGRTE 180 : |:|: : :| : :|
                                                                                                                                                                                                                                                                                                                                                                                                                         YHTYGPHS-----CHIP-KDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HQAPTARGAVRFWCSLPTADTSSFVPLELRVTAAS--GAPRYH-RVIHINEVVLLDAPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVNISCWSKNMKDLTCRWT------PGAHGETFLHTNYSLKYKLR---WYGQDNTCEE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSV-----DWKVVDDVSNQTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P16471; 1BP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR002996; CR1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           · 2
2
                   Chordata; Crania
Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46315 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.4%;
26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FN_III.
                                                                                           05, Created)
05, Last sequence update)
19, Last annotation updat
                                                                             FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 159.5;
Pred. No. 7.3
               Craniata; Vertebrat
actyla; Ruminantia;
                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0D2C5F7A01B942EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                           296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            422
                                   Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .3e-07;
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                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84;
                       Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69
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RESULTA

Q304584

ID

Q60

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Best Local S
Matches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O9JM58, PRELIMINARY;
O9JM58,
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Hiroyama T., Iwama A., Nakamura Y., I

"Cytokine receptor like molecule 3."

Submitted (MAR-2000) to the EMBL/Genl

EMBL; AB040038; BAA92777.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOKINE RECEPTOR LIKE CRLF1 OR CRLM3.
                                                                                                                                                                                                                                                    MGD;
                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endocrinology 138:3187-3194(1997).
EMBL; AF027403; AAB83999.1; -.
HSSP; P14787; 1AN3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-97375450; PubMed-9231767;
Schuler L.A., Nagel R.J., Gao J.,
"Prolactin receptor heterogeneity"
                                                                                                                           Signal; Receptor.
SIGNAL 1
                                                                                                                                                                                  InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III
Pfam; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                 SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
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rPro; IPR003528; 1
; PF00041; fn3; 2
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                                                                                                                                                                                                                                                MGI:1340030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLTLELKHPEDRKPYLWIKWSPPTMTDVKSGWFIIQYEIRLKPEKATDWETHFTLKQ--T
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                                                                                                                                                                                                                                                                     P16471; 1BP3
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E; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
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                     Similarity
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    Conservative
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                                                                                                      34
46662 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
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2.
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                       13
25
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Hematopo_receptor_L_F1.
                       . 28;
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    29;
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Score 157.5;
Pred. No. 1.1e
29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 159; DB
Pred. No. 5.2e.
36; Mismatches
                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases
                                                                                                 POTENTIAL.
; 910535C629CA7056 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                       .1e-06;
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.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₿
                                        DB 11;
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l and maternal
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                                      Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
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-i- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED (1 PITUITARY, ADRENAL GLAND, OVARY AND ETTAL LIVER).
-i- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-i- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS EMBL; AF041297; AAB96795.1; -.
EMBL; AF041979; AAB96020.1; -.
EMBL; AF041979; AAB97082.1; -.
EMBL; AF042358; AAB97744.1; -.
EMBL; AF042358; AAB97743.1; -.
EMBL; AF042358; AAB97743.1; -.
EMBL; AF041978; AAB9665.1; -.
EMBL; AF041978; AAB96965.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bignon C., Binart N., Ormandy C., Schuler L.A., Kelly P.A., Djiane "Long and short forms of the ovine prolactin receptor: cDNA clonify and genomic analysis reveal that the two forms arise by different alternative splicing mechanisms in ruminants and in rodents."; J. Mol. Endocrinol. 19:109-120(1997).
                                                                                                                                                                                                                              -i- SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- ALTERNATIVE PRODUCTS: THREE ISOFORMS; LONG ISOFORM
                                                                                                                                                                                                                                                                                                  Anthony R.V., Smith G.W., Duong A., Pratt S.L., Smith M.F., "Two forms of the prolactin receptor messenger ribonucleic present in ovine fetal liver and adult ovary."; Endocrine 3:291-295(1995).
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 147-302 FROM N.A., AND ALTERNATIVE TISSUE=FETAL LIVER, AND CORPUS LUTEUM;
                                                                                                                                                                                                                                                                                                                                                                                                                      "Detection of prolactin receptor gene expression i pituitary gland and visualization of the specific signal in gonadotrophs."; Endocrinology 139:5215-5223(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99049302; PubMed=9832462; Tortonese D.J., Brooks J., Ingleton P.M., McNeilly A.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 61-395 FROM N.A., AND ALTERNATIVE SPLICING.
STRAIN-SCOTTISH BLACKFACE / ISOLATE M22/80; TISSUE-ANTERIOR PITUITARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
Bovidae; Caprinae; (
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                -i- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PROLACTIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                    TISSUE=FETAL LIVER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98001468;
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                                                                                                                                                                                             ALTERNATIVE SPLICING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L-VARLADESGHVVLRWLPPPET----PMTSHIRYEVDVSAGNGAGSVQRVEILEGRTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VHVSRVGGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSV----
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                                                                                                                                                                                                              SHORT ISOFORM (S-OPR) AND
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                                                                                                                                                                                                                                                                                  PITUITARY
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VARSPLIC
Yamamoto.T., Nakayama Y., Matsuda Y., Abe S.-I.; "Cloning and expression of a cDNA encoding a prolactin Japanese red-bellied newt, Cynops pyrrhogaster."; Zool. Sci. 15:741-747(1998).
                                                                                                                               Q90WG7;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
PROLACTIN RECEPTOR PRECURSOR.
                                                                                            Cynops pyrrhogaster (Japanese common newt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cyno
                                                 TISSUE=KIDNEY;
                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                          Q90WG7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                 131
                                                                                                                                                                                                                                                    189
                                                                                                                                                                                                                                                                                                                        125
                                                                                                                                                                                                                                                                                                                                                74
                                                                                                                                                                                                                                                                                                                                                                      71
                                                                                                                                                                                                                                                                                                                                                                                              19
                                                                                                                                                                                                                                                                                                                                                                                                                  15 AALLAARGPEE----LLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLH
                                                                                                                                                                                                                 13
                                                                                                                                                                                                                                                                                                                                                                      QAPTARGAVRFWCSLPTADTSSFVPLELRVTA-----ASGAPRYHRVIHINEVVLLDAP
                                                                                                                                                                                                                                                  TQLKIFNLYPGQKYLVQIRCK---PDH-GYWSEWSPESFIQIPND
                                                                                                                                                                                                                                                                          TECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSD
                                                                                                                                                                                                                                                                                                VNLTLELKHPEDRKPYLWIKWSPPTLTDVKSGWFSIQYEIRLKPEKATD--WETHFAPKL
                                                                                                                                                                                                                                                                                                                       VGLVARL---ADESGHVVLRWLPPPETPMTS---HIRYEVDVSAGNGAGSVQRVEILEGR
                                                                                                                                                                                                                                                                                                                                                ECPDYKTGGPNSCYFSKKYTSIWKMYVITVSAINQMGISSSDPLY
                                                                                                                                                                                                                                                                                                                                                                                             ASLLNGQSPPEKPKLIKCRSPGKETFTCWWEPGADGGL-PTNYTLTYRKEGE----TLIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00041; fn3; ; ; SM00060; FN3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y10808; CAA71766.1;
P14787; 1AN3.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR003528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    re splicing.
24
25
581
25
581
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73
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182
3
27
46
86
86
86
10
132
N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR003961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR002996; CR1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297
281
                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              581
281
387
65235 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEMATOPO_REC_L_F1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          581
296
                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.6%;
24.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hematopo_receptor_L_F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                          36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISOFORM).
MISSING (
I -> V (I
E -> K (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 151; DB 6;
Pred. No. 6.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

QOSPPEKPKLIKCRSPCKETFTCWWEDGADGGLPTMYLTY

RK -> ASLYVPGGKCSSVCTYMAYPFVGGIFLHMYLCVDQ

YLLLTYTS (IN SOLUBLE ISOFORM).

MISSING (IN SOLUBLE ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGKSEELLRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROLACTIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISSING (IN SHORT ISOFORM).

-> V (IN AAB97743 AND AAB97744).

-> K (IN REF. 2).

EC534FDE538837A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNKNOWN_1
                                                                                                                                                                                          626
                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> ISQPSRLVSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                            104;
                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                ---VDVTYIVEPEPP
                                                                                                                                                                                                                                                    229
                          receptor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΩIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHORT
                                                                                              Cynops
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   70
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RESULT
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뭥
                                                                                          Query Match
Best Local S
Matches 51
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB005045; BA
Signal; Receptor.
SIGNAL 1
SEQUENCE 626 AA;
                                                                                                                                                    Receptor.
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                           Howell-Skalla L.A., Bunick D., Bleck G.T., Nelson R.A., Bahr J.M. "Cloning and sequence analysis of the extracellular region of th polar bear (Ursus maritimus) luteinizing hormone receptor (LHF), follicle stimulating hormone receptor (FSHr), and prolactin rece (PRLr) genes and their expression in the testis of the black bea
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                           Ursus maritimus (Polar bear) (Thalarctos maritimus). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9GLW3
                                                                                                                                                                                                   SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20086658; PubMed=10618652;
                                                                                                                                                                                                                                                                                                                                                                   TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=29073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROLACTIN RECEPTOR (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9GLW3;
                                                                                                                                                                                                             InterPro; IPRO
Pfam; PF00041;
                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                  (Ursus americanus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187
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57
                       94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23
                                              N
                                                                                                                                                                                                                                              Reprod. Dev. 55:136-145(2000).; AF169792; AAG10648.1; -...; P14787; 1AN3.
TMYIITINATNQMGSSSSDPRY--
                                                           EDLYCFWEEAASAGYGPGNYSFSYQLEDEPWKLCRLHQAPTARGAYRFWCSLPTADTSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NPSENYIVQVRCK----SDHGFWSMWSPESYIQIPDN 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HVVLRWLPPPETPMTS----HIRYEVDVSAGNG-----AGSVQRVEILEGRTECVLSNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CFFDKKHTSIWTMYNIIVNATNELGSTTSDPKF----VDVAYIVQLRPPLNVTLSIIYEPP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSLPTADTSSFVPLELRVTA-----ASGAPRYHRVIHINEVVLLDAPVGLVARLADESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVNIMCRSPEKETFSCWWQPGSDGGL-PTNYSLLYKTEGKN----TYSECPDYKTSGPNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFW
                       VPLELRVTA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLLVKWSPPSEADVKSGWVTIEYEVQFKSKKAKEWETLTAGKQRQLKVF--
                                              ETFTCWWKPGEDGGL-PTNYTLTYRKEGE---
                                                                                          Similarity 24.:
51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                            IPR002996; CR1A.
IPR003961; FN_III
0041; fn3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       626 AA;
                                                                                                                                                    227
227
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                     A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAB61107.1;
                                                                                                                                                    227
26114 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 F
69944 MW;
                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata;
Carnivora; Fissipedia; Ursidae;
                      -ASGAPRYHRVIHINEVVLLDAPVGLVARL---ADESGHVVLRWLP 144
                                                                                                      11.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              16,
19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence up
                                                                                        Score 140; DB
Pred. No. 2.3e
33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
; B6050DD9C9F58DE5 CRC64;
 -VDVTYIVEPDPPVNLTLELKQPEDKKPYLWMKWYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                     F5E6C5F33B5D5B49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140.5;
No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227
                                             -TTTHECPDYISSGPNSCYFNKKHTSIW
                                                                                          DB 6;
2.3e-05;
tes 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .3e-05;
es 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                               Length
                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi; Ursus.
                                                                                                                   227;
                                                                                                                                                                                                                                                                                                black bear
                                                                                                                                                                                                                                                                                                                                              Bahr J.M.;
                                                                                             40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37;
                                                                                                                                                                                                                                                                                                                                  the
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                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186
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                                              56
                                                                      93
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                                                                                             10;
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Qy
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Search completed: August 28, Job time: 546 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The prolactin receptor from the brushtail possum (Trichosurus vulpecula): cDNA cloning, expression and functional analysis."; wol. Cell. Endocrinol. 148:119-127(1999).

EMBL; AF098296; AAD27039.1; -.

HSSP; P14787; 1AN3;
InterPro; IPR003296; CR1A.
InterPro; IPR003296; FN_III.
InterPro; IPR003961; FN_III.
InterPro; IPR003961; FN_III.
START; SMOUDGO; FN3; 1.
PROSSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9XS92 PRELIMINARY; PRT; 625 AA. Q9XS92; 01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) PROLACTIN RECEPTOR PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01352;
Signal; Receptor.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trichosurus vulpecula (Brush-tailed possum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Metatheria; Diprotodontia; Phalangeridae;
NCBI_TaxID=9337;
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Demmer J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99236966; PubMed=10221777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=TESTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 QVRCK---PDH-GFWSEWSPESSIQIPNDV 190
                                                                            187
                                                                                                                                       129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114
                                                                                                     177 GRTECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSDL 224
                                                                                                                                                                123 APVGL---VARLADESGHVVLRWLPPPETPMTS---HIRYEVDVSAGNGAGSVQRVEILE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 AVRARMAEPSFGGFWSAWSEPVSLLTPSDL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 PPETPMTS---HIRYEVDVSAGNG------AGSVQRVEILEGRTECVLSNLRGRTRYTF 194
                                                                                                                                                                                                                69 LHQAPTARGAVRFWCSLPTADTSSFVPLELRVTAAS-----GAPRYHRVIHINEVVLLD 122
                                                                                                                                                                                                                                                        72 THECPDYKTGGPNSCYFNKKHTSIWMVYIIWVNATNQMGRSMSEPRY---VDVTYIVEPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                         PKFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDEPWKLCR 68
                                                                         QQTQFKIFSLYLGQKYLVEVRCK---PDHGS-WSQWSPESSILIPSDI 230
                                                                                                                                   PPLNLTLEVKQPEDGKPYLWLKWSPPVLVDVRSGWLTLQYELRLKPEKAA--EWETHFAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTLVDVRSGWLTLQYEIRLKPEKATEWETHFAGQQTQFKIL-----SLYPGQKYLV 164
                                                                                                                                                                                                                                                                                                                                                                                                  25
625 AA;
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                             24 POTENTIAL.
625 PROLACTIN RECEPTOR.
70539 MW; 2097D72827C9DBB6 CRC64;
                                                                                                                                                                                                                                                                                                                    11.6%; Score 139; DB 6; Length 625; 24.6%; Pred. No. 0.0001; ative 34; Mismatches 98; Indels
              2002, 17:40:15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
Trichosurus.
                                                                                                                                                                                                                                                                                                                      40;
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                     186
                                                                                                                                                                                                128
                                                                                                                                                                                                                                                                                                                      11;
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